# Phyre$^2$

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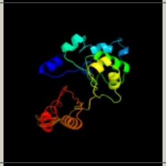
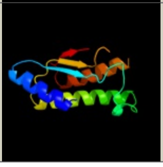
| Description | P75746 |
| Date | Thu Jan 5 12:13:43 GMT 2012 |
| Unique Job ID | 32ebaa6d1c8841af |

Detailed template information

| # | Template | Alignment Coverage | 3D Model | Confidence | % i.d. | Template Information |
|---|---|---|---|---|---|---|
| 1 | d2dfaa1 | Alignment |  | 100.0 | 46 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**Glycoside hydrolase/deacetylase<br>**Family:**LamB/YcsF-like |
| 2 | d1v6ta_ | Alignment |  | 100.0 | 43 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**Glycoside hydrolase/deacetylase<br>**Family:**LamB/YcsF-like |
| 3 | c2x5eA_ | Alignment |  | 100.0 | 39 | **PDB header:**unknown function<br>**Chain:** A: **PDB Molecule:**upf0271 protein pa4511;<br>**PDBTitle:** crystal structure of the hypothetical protein pa4511 from2 pseudomonas aeruginosa |
| 4 | d1xw8a_ | Alignment |  | 100.0 | 95 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**Glycoside hydrolase/deacetylase<br>**Family:**LamB/YcsF-like |
| 5 | d2nlya1 | Alignment |  | 91.1 | 16 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**Glycoside hydrolase/deacetylase<br>**Family:**Divergent polysaccharide deacetylase |
| 6 | c2c1iA_ | Alignment |  | 89.5 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**peptidoglycan glcnac deacetylase;<br>**PDBTitle:** structure of streptococcus pnemoniae peptidoglycan2 deacetylase (sppgda) d 275 n mutant. |
| 7 | d1ny1a_ | Alignment |  | 87.4 | 15 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**Glycoside hydrolase/deacetylase<br>**Family:**NodB-like polysaccharide deacetylase |
| 8 | d1tz9a_ | Alignment |  | 84.1 | 16 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**UxuA-like |
| 9 | c1w17A_ | Alignment |  | 79.9 | 17 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**probable polysaccharide deacetylase pdaa;<br>**PDBTitle:** structure of bacillus subtilis pdaa, a family 42 carbohydrate esterase. |
| 10 | c2qv5A_ | Alignment |  | 65.7 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein atu2773;<br>**PDBTitle:** crystal structure of uncharacterized protein atu2773 from2 agrobacterium tumefaciens c58 |
| 11 | d1ur4a_ | Alignment |  | 65.4 | 22 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**beta-glycanases |

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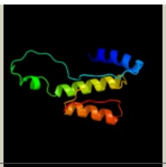
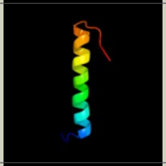
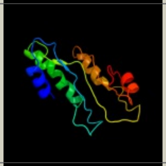
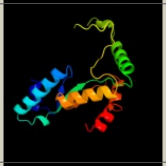
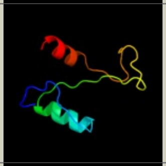
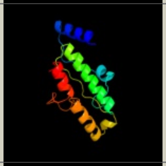
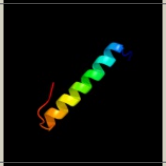
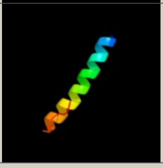
| 12 | d2fvka2 | Alignment |  | 62.4 | 28 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Metallo-dependent hydrolases<br>**Family:**Hydantoinase (dihydropyrimidinase), catalytic domain |
| 13 | c1e9zA_ | Alignment |  | 58.9 | 25 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**urease subunit alpha;<br>**PDBTitle:** crystal structure of helicobacter pylori urease |
| 14 | c1w8gA_ | Alignment |  | 58.5 | 12 | **PDB header:**plp-binding protein<br>**Chain:** A: **PDB Molecule:**hypothetical upf0001 protein yggs;<br>**PDBTitle:** crystal structure of e. coli k-12 yggs |
| 15 | c1tvlA_ | Alignment |  | 58.1 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**protein ytnj;<br>**PDBTitle:** structure of ytnj from bacillus subtilis |
| 16 | d1tvla_ | Alignment |  | 58.1 | 21 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Bacterial luciferase-like<br>**Family:**Ssud-like monoxygenases |
| 17 | c3e0fA_ | Alignment |  | 57.3 | 18 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**putative metal-dependent phosphoesterase;<br>**PDBTitle:** crystal structure of a putative metal-dependent phosphoesterase2 (bad_1165) from bifidobacterium adolescentis atcc 15703 at 2.40 a3 resolution |
| 18 | c3qxbB_ | Alignment |  | 56.5 | 15 | **PDB header:**isomerase<br>**Chain:** B: **PDB Molecule:**putative xylose isomerase;<br>**PDBTitle:** crystal structure of a putative xylose isomerase (yp_426450.1) from2 rhodospirillum rubrum atcc 11170 at 1.90 a resolution |
| 19 | d1e9ya2 | Alignment |  | 56.2 | 25 | **Fold:**Urease, gamma-subunit<br>**Superfamily:**Urease, gamma-subunit<br>**Family:**Urease, gamma-subunit |
| 20 | d1ejxa_ | Alignment |  | 54.4 | 22 | **Fold:**Urease, gamma-subunit<br>**Superfamily:**Urease, gamma-subunit<br>**Family:**Urease, gamma-subunit |
| 21 | d4ubpa_ | Alignment | not modelled | 52.9 | 19 | **Fold:**Urease, gamma-subunit<br>**Superfamily:**Urease, gamma-subunit<br>**Family:**Urease, gamma-subunit |
| 22 | c3tsuA_ | Alignment | not modelled | 51.3 | 23 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**transcriptional regulatory protein;<br>**PDBTitle:** crystal structure of e. coli hypf with amp-pnp and carbamoyl phosphate |
| 23 | c1y10C_ | Alignment | not modelled | 50.0 | 11 | **PDB header:**lyase<br>**Chain:** C: **PDB Molecule:**hypothetical protein rv1264/mt1302;<br>**PDBTitle:** mycobacterial adenylyl cyclase rv1264, holoenzyme, inhibited state |
| 24 | c2o7jA_ | Alignment | not modelled | 47.5 | 13 | **PDB header:**sugar binding protein<br>**Chain:** A: **PDB Molecule:**oligopeptide abc transporter, periplasmic<br>**PDBTitle:** the x-ray crystal structure of a thermophilic cellobiose2 binding protein bound with cellopentaose |
| 25 | c3noyA_ | Alignment | not modelled | 45.8 | 25 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase;<br>**PDBTitle:** crystal structure of ispg (gcpe) |
| 26 | d2nu7b1 | Alignment | not modelled | 43.1 | 17 | **Fold:**Flavodoxin-like<br>**Superfamily:**Succinyl-CoA synthetase domains<br>**Family:**Succinyl-CoA synthetase domains |
| 27 | c3bdkB_ | Alignment | not modelled | 43.0 | 26 | **PDB header:**lyase<br>**Chain:** B: **PDB Molecule:**d-mannonate dehydratase;<br>**PDBTitle:** crystal structure of streptococcus suis mannonate2 dehydratase complexed with substrate analogue |
| 28 | c2hk1D_ | Alignment | not modelled | 42.5 | 13 | **PDB header:**isomerase<br>**Chain:** D: **PDB Molecule:**d-psicose 3-epimerase;<br>**PDBTitle:** crystal structure of d-psicose 3-epimerase (dpease) in the presence of2 d-fructose |

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| 29 | d1hara_ | Alignment | not modelled | 42.0 | 7 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**Reverse transcriptase |
| 30 | c2e67D_ | Alignment | not modelled | 38.5 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** D: **PDB Molecule:**hypothetical protein tthb029;<br>**PDBTitle:** crystal structure of the hypothetical protein tthb029 from thermus2 thermophilus hb8 |
| 31 | c3epmB_ | Alignment | not modelled | 38.0 | 20 | **PDB header:**biosynthetic protein<br>**Chain:** B: **PDB Molecule:**thiamine biosynthesis protein thic;<br>**PDBTitle:** crystal structure of caulobacter crescentus thic |
| 32 | c2ou4C_ | Alignment | not modelled | 37.3 | 15 | **PDB header:**isomerase<br>**Chain:** C: **PDB Molecule:**d-tagatose 3-epimerase;<br>**PDBTitle:** crystal structure of d-tagatose 3-epimerase from2 pseudomonas cichorii |
| 33 | d1xima_ | Alignment | not modelled | 36.8 | 28 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 34 | c2pfsA_ | Alignment | not modelled | 35.6 | 13 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**universal stress protein;<br>**PDBTitle:** crystal structure of universal stress protein from nitrosomonas2 europaea |
| 35 | d1nq6a_ | Alignment | not modelled | 34.9 | 13 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**beta-glycanases |
| 36 | c3hgmD_ | Alignment | not modelled | 33.7 | 14 | **PDB header:**signaling protein<br>**Chain:** D: **PDB Molecule:**universal stress protein tead;<br>**PDBTitle:** universal stress protein tead from the trap transporter2 teaabc of halomonas elongata |
| 37 | d1qt1a_ | Alignment | not modelled | 33.3 | 23 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 38 | d1qyia_ | Alignment | not modelled | 31.7 | 12 | **Fold:**HAD-like<br>**Superfamily:**HAD-like<br>**Family:**Hypothetical protein MW1667 (SA1546) |
| 39 | d1eucb1 | Alignment | not modelled | 31.7 | 18 | **Fold:**Flavodoxin-like<br>**Superfamily:**Succinyl-CoA synthetase domains<br>**Family:**Succinyl-CoA synthetase domains |
| 40 | c3qgaD_ | Alignment | not modelled | 31.0 | 23 | **PDB header:**hydrolase<br>**Chain:** D: **PDB Molecule:**fusion of urease beta and gamma subunits;<br>**PDBTitle:** 3.0 a model of iron containing urease urea2b2 from helicobacter2 mustelae |
| 41 | c3mvnA_ | Alignment | not modelled | 29.1 | 13 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**udp-n-acetylmuramate:l-alanyl-gamma-d-glutamyl-medo-<br>**PDBTitle:** crystal structure of a domain from a putative udp-n-acetylmuramate:l-2 alanyl-gamma-d-glutamyl-medo-diaminopimelate ligase from haemophilus3 ducreyi 35000hp |
| 42 | d1v6wa2 | Alignment | not modelled | 28.2 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**beta-glycanases |
| 43 | d1xlma_ | Alignment | not modelled | 27.6 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 44 | d1ulza2 | Alignment | not modelled | 26.2 | 25 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**BC N-terminal domain-like |
| 45 | d2j9ga2 | Alignment | not modelled | 25.7 | 25 | **Fold:**PreATP-grasp domain<br>**Superfamily:**PreATP-grasp domain<br>**Family:**BC N-terminal domain-like |
| 46 | c3c6cA_ | Alignment | not modelled | 25.4 | 14 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**3-keto-5-aminohexanoate cleavage enzyme;<br>**PDBTitle:** crystal structure of a putative 3-keto-5-aminohexanoate cleavage2 enzyme (reut_c6226) from ralstonia eutropha jmp134 at 1.72 a3 resolution |
| 47 | c3louB_ | Alignment | not modelled | 24.8 | 23 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase;<br>**PDBTitle:** crystal structure of formyltetrahydrofolate deformylase (yp_105254.1)2 from burkholderia mallei atcc 23344 at 1.90 a resolution |
| 48 | d2c1ia1 | Alignment | not modelled | 24.7 | 16 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**Glycoside hydrolase/deacetylase<br>**Family:**NodB-like polysaccharide deacetylase |
| 49 | c1k97A_ | Alignment | not modelled | 24.6 | 16 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**argininosuccinate synthase;<br>**PDBTitle:** crystal structure of e. coli argininosuccinate synthetase in complex2 with aspartate and citrulline |
| 50 | c3bzjA_ | Alignment | not modelled | 24.5 | 16 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**uv endonuclease;<br>**PDBTitle:** uvde k229l |
| 51 | d1ur1a_ | Alignment | not modelled | 24.0 | 15 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**beta-glycanases |
| 52 | d2glka1 | Alignment | not modelled | 23.6 | 24 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 53 | c3sg0A_ | Alignment | not modelled | 23.5 | 12 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**extracellular ligand-binding receptor;<br>**PDBTitle:** the crystal structure of an extracellular ligand-binding receptor from2 rhodopseudomonas palustris haa2 |
|  |  |  |  |  |  | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**adenylate/guanylate cyclase/hydrolase, |

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| 54 | c3mr7B_ | Alignment | not modelled | 23.1 | 17 | alpha/beta fold<br>**PDBTitle:** crystal structure of adenylate/guanylate cyclase/hydrolase from2 silicibacter pomeroyi |
| 55 | d1zvpa2 | Alignment | not modelled | 22.1 | 27 | **Fold:**Ferredoxin-like<br>**Superfamily:**ACT-like<br>**Family:**VC0802-like |
| 56 | c3chvA_ | Alignment | not modelled | 21.7 | 23 | **PDB header:**metal binding protein<br>**Chain:** A: **PDB Molecule:**prokaryotic domain of unknown function (duf849) with a tim<br>**PDBTitle:** crystal structure of a prokaryotic domain of unknown function (duf849)2 member (spoa0042) from silicibacter pomeroyi dss-3 at 1.45 a3 resolution |
| 57 | c3ugsB_ | Alignment | not modelled | 21.4 | 11 | **PDB header:**transferase<br>**Chain:** B: **PDB Molecule:**undecaprenyl pyrophosphate synthase;<br>**PDBTitle:** crystal structure of a probable undecaprenyl diphosphate synthase2 (upps) from campylobacter jejuni |
| 58 | c3n2aA_ | Alignment | not modelled | 21.4 | 17 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**bifunctional folylpolyglutamate synthase/dihydrofolate<br>**PDBTitle:** crystal structure of bifunctional folylpolyglutamate2 synthase/dihydrofolate synthase from yersinia pestis co92 |
| 59 | c2dclB_ | Alignment | not modelled | 21.1 | 23 | **PDB header:**structural genomics, unknown function<br>**Chain:** B: **PDB Molecule:**hypothetical upf0166 protein ph1503;<br>**PDBTitle:** structure of ph1503 protein from pyrococcus horikoshii ot3 |
| 60 | d1uasa2 | Alignment | not modelled | 21.0 | 8 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Amylase, catalytic domain |
| 61 | d1hl9a2 | Alignment | not modelled | 20.8 | 10 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**(Trans)glycosidases<br>**Family:**Putative alpha-L-fucosidase, catalytic domain |
| 62 | c3tpaA_ | Alignment | not modelled | 20.4 | 9 | **PDB header:**heme binding protein<br>**Chain:** A: **PDB Molecule:**heme-binding protein a;<br>**PDBTitle:** structure of hbpa2 from haemophilus parasuis |
| 63 | c3o1lB_ | Alignment | not modelled | 20.1 | 14 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**formyltetrahydrofolate deformylase;<br>**PDBTitle:** crystal structure of a formyltetrahydrofolate deformylase (pspto_4314)2 from pseudomonas syringae pv. tomato str. dc3000 at 2.20 a resolution |
| 64 | d1abra_ | Alignment | not modelled | 20.1 | 15 | **Fold:**Ribosome inactivating proteins (RIP)<br>**Superfamily:**Ribosome inactivating proteins (RIP)<br>**Family:**Plant cytotoxins |
| 65 | c1ygyA_ | Alignment | not modelled | 20.1 | 21 | **PDB header:**oxidoreductase<br>**Chain:** A: **PDB Molecule:**d-3-phosphoglycerate dehydrogenase;<br>**PDBTitle:** crystal structure of d-3-phosphoglycerate dehydrogenase from2 mycobacterium tuberculosis |
| 66 | c2i7xA_ | Alignment | not modelled | 19.9 | 21 | **PDB header:**rna binding protein, protein binding<br>**Chain:** A: **PDB Molecule:**protein cft2;<br>**PDBTitle:** structure of yeast cpsf-100 (ydh1p) |
| 67 | d2i7xa1 | Alignment | not modelled | 19.9 | 21 | **Fold:**Metallo-hydrolase/oxidoreductase<br>**Superfamily:**Metallo-hydrolase/oxidoreductase<br>**Family:**beta-CASP RNA-metabolising hydrolases |
| 68 | d1st6a4 | Alignment | not modelled | 19.8 | 25 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**alpha-catenin/vinculin-like<br>**Family:**alpha-catenin/vinculin |
| 69 | c3cpgA_ | Alignment | not modelled | 19.8 | 12 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**uncharacterized protein;<br>**PDBTitle:** crystal structure of an unknown protein from bifidobacterium2 adolescentis |
| 70 | d2gc6a1 | Alignment | not modelled | 19.7 | 17 | **Fold:**MurD-like peptide ligases, peptide-binding domain<br>**Superfamily:**MurD-like peptide ligases, peptide-binding domain<br>**Family:**Folylpolyglutamate synthetase, C-terminal domain |
| 71 | c3fh0A_ | Alignment | not modelled | 19.3 | 15 | **PDB header:**structural genomics, unknown function<br>**Chain:** A: **PDB Molecule:**putative universal stress protein kpn_01444;<br>**PDBTitle:** crystal structure of putative universal stress protein kpn_01444 -2 atpase |
| 72 | c3t0nA_ | Alignment | not modelled | 19.2 | 10 | **PDB header:**signaling protein<br>**Chain:** A: **PDB Molecule:**twin-arginine translocation pathway signal;<br>**PDBTitle:** crystal structure of twin-arginine translocation pathway signal from2 rhodopseudomonas palustris bisb5 |
| 73 | c2fvhB_ | Alignment | not modelled | 18.9 | 29 | **PDB header:**hydrolase<br>**Chain:** B: **PDB Molecule:**urease gamma subunit;<br>**PDBTitle:** crystal structure of rv1848, a urease gamma subunit urea (urea2 amidohydrolase), from mycobacterium tuberculosis |
| 74 | d1pb5a_ | Alignment | not modelled | 18.6 | 60 | **Fold:**Notch domain<br>**Superfamily:**Notch domain<br>**Family:**Notch domain |
| 75 | c1w96B_ | Alignment | not modelled | 18.6 | 11 | **PDB header:**ligase<br>**Chain:** B: **PDB Molecule:**acetyl-coenzyme a carboxylase;<br>**PDBTitle:** crystal structure of biotin carboxylase domain of acetyl-2 coenzyme a carboxylase from saccharomyces cerevisiae in3 complex with soraphen a |
| 76 | c2xzmO_ | Alignment | not modelled | 18.4 | 15 | **PDB header:**ribosome<br>**Chain:** O: **PDB Molecule:**rps13e;<br>**PDBTitle:** crystal structure of the eukaryotic 40s ribosomal2 subunit in complex with initiation factor 1. this file3 contains the 40s subunit and initiation factor for4 molecule 1 |
| 77 | d1bxca_ | Alignment | not modelled | 18.3 | 28 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**Xylose isomerase |
| 78 | c3la4A_ | Alignment | not modelled | 18.2 | 31 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**urease;<br>**PDBTitle:** crystal structure of the first plant urease from jack bean |

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| | | | | | | (canavalia2 ensiformis) |
| 79 | d1i60a_ | Alignment | not modelled | 18.0 | 17 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Xylose isomerase-like<br>**Family:**IolI-like |
| 80 | c3sdoB_ | Alignment | not modelled | 17.9 | 16 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**nitrilotriacetate monooxygenase;<br>**PDBTitle:** structure of a nitrilotriacetate monooxygenase from burkholderia2 pseudomallei |
| 81 | d1st6a3 | Alignment | not modelled | 17.8 | 15 | **Fold:**Four-helical up-and-down bundle<br>**Superfamily:**alpha-catenin/vinculin-like<br>**Family:**alpha-catenin/vinculin |
| 82 | c3dddA_ | Alignment | not modelled | 17.7 | 11 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**putative acetyltransferase;<br>**PDBTitle:** crystal structure of a putative acetyltransferase (np_142035.1) from2 pyrococcus horikoshii at 2.25 a resolution |
| 83 | c1kh2D_ | Alignment | not modelled | 17.5 | 24 | **PDB header:**ligase<br>**Chain:** D: **PDB Molecule:**argininosuccinate synthetase;<br>**PDBTitle:** crystal structure of thermus thermophilus hb82 argininosuccinate synthetase in complex with atp |
| 84 | c3civA_ | Alignment | not modelled | 17.5 | 15 | **PDB header:**hydrolase<br>**Chain:** A: **PDB Molecule:**endo-beta-1,4-mannanase;<br>**PDBTitle:** crystal structure of the endo-beta-1,4-mannanase from2 alicyclobacillus acidocaldarius |
| 85 | c3ue9A_ | Alignment | not modelled | 17.4 | 18 | **PDB header:**ligase<br>**Chain:** A: **PDB Molecule:**adenylosuccinate synthetase;<br>**PDBTitle:** crystal structure of adenylosuccinate synthetase (ampsase) (pura) from2 burkholderia thailandensis |
| 86 | d1nfpa_ | Alignment | not modelled | 17.0 | 19 | **Fold:**TIM beta/alpha-barrel<br>**Superfamily:**Bacterial luciferase-like<br>**Family:**Non-fluorescent flavoprotein (luxF, FP390) |
| 87 | d2fdra1 | Alignment | not modelled | 16.9 | 13 | **Fold:**HAD-like<br>**Superfamily:**HAD-like<br>**Family:**beta-Phosphoglucomutase-like |
| 88 | d1o94c_ | Alignment | not modelled | 16.5 | 15 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**ETFP subunits |
| 89 | d1efpb_ | Alignment | not modelled | 16.4 | 16 | **Fold:**Adenine nucleotide alpha hydrolase-like<br>**Superfamily:**Adenine nucleotide alpha hydrolases-like<br>**Family:**ETFP subunits |
| 90 | c3t66A_ | Alignment | not modelled | 16.1 | 27 | **PDB header:**transport protein<br>**Chain:** A: **PDB Molecule:**nickel abc transporter (nickel-binding protein);<br>**PDBTitle:** crystal structure of nickel abc transporter from bacillus halodurans |
| 91 | c3ly1C_ | Alignment | not modelled | 16.0 | 19 | **PDB header:**transferase<br>**Chain:** C: **PDB Molecule:**putative histidinol-phosphate aminotransferase;<br>**PDBTitle:** crystal structure of putative histidinol-phosphate aminotransferase2 (yp_050345.1) from erwinia carotovora atroseptica scri1043 at 1.80 a3 resolution |
| 92 | d2c71a1 | Alignment | not modelled | 15.9 | 21 | **Fold:**7-stranded beta/alpha barrel<br>**Superfamily:**Glycoside hydrolase/deacetylase<br>**Family:**NodB-like polysaccharide deacetylase |
| 93 | d1gvia2 | Alignment | not modelled | 15.5 | 30 | **Fold:**Glycosyl hydrolase domain<br>**Superfamily:**Glycosyl hydrolase domain<br>**Family:**alpha-Amylases, C-terminal beta-sheet domain |
| 94 | d1ztwa1 | Alignment | not modelled | 15.4 | 11 | **Fold:**DNA/RNA polymerases<br>**Superfamily:**DNA/RNA polymerases<br>**Family:**Reverse transcriptase |
| 95 | d2pw6a1 | Alignment | not modelled | 15.4 | 20 | **Fold:**Phosphorylase/hydrolase-like<br>**Superfamily:**LigB-like<br>**Family:**LigB-like |
| 96 | c3elyA_ | Alignment | not modelled | 15.2 | 18 | **PDB header:**transferase<br>**Chain:** A: **PDB Molecule:**methyltransferase;<br>**PDBTitle:** wesselsbron virus methyltransferase in complex with adohcy |
| 97 | d8ruca2 | Alignment | not modelled | 15.1 | 24 | **Fold:**Ferredoxin-like<br>**Superfamily:**RuBisCO, large subunit, small (N-terminal) domain<br>**Family:**Ribulose 1,5-bisphosphate carboxylase-oxygenase |
| 98 | c2c2xB_ | Alignment | not modelled | 14.8 | 20 | **PDB header:**oxidoreductase<br>**Chain:** B: **PDB Molecule:**methylenetetrahydrofolate dehydrogenase-<br>**PDBTitle:** three dimensional structure of bifunctional2 methylenetetrahydrofolate dehydrogenase-cyclohydrolase3 from mycobacterium tuberculosis |
| 99 | c2grvC_ | Alignment | not modelled | 14.7 | 14 | **PDB header:**biosynthetic protein<br>**Chain:** C: **PDB Molecule:**lpqw;<br>**PDBTitle:** crystal structure of lpqw |